Appl. No. 09/990,046
Amend. dated March 21, 2005
Response to Office Action mailed on: December 20, 2004

Patent Docket **P1405R1C1**

REMARKS

Formal Matters

A substitute specification, revised sequence listing and formal drawings are provided in order to correct various errors of form. Responsive to the Examiner's remark concerning the priority information, the paragraph at page 1, line 12 has been appropriately revised.

In amended Figures 1A-1E, Figures 2A-2B, Figures 3A-3D, Figure 4, Figure 5, Figures 6A-6F, Figure 7A-7B, Figures 8A-8D, Figure 9, Figure 10A-10D and Figure 11A-B, extraneous text was removed from the Figures.

Claims 29-54 remain in this application. No claim has been canceled. Claims 29, 39 and 49 are amended. No new matter is added by the amendments.

Support for the amendments to claims 29, 39, 49 is found at least at page 49, lines 33-36.

In view of the Examiner's earlier 6-way restriction requirement in parent application USSN 09/292,505, now U.S.P. 6,348,575, applicant retains the right to present previously withdrawn and cancelled claims in a divisional application.

The Rejection under 35 U.S.C. § 101

Claims 29-34, 37, 39-44, 47, 49-50 and 53 are rejected under 35 U.S.C. § 101 allegedly for being directed to non-statutory subject matter.

In response, Applicants amendment renders the rejection moot.

The Rejection under 35 U.S.C. § 102(e)

Claims 29-35, 37-45, 47-51, and 53-54 are rejected under 35 U.S.C. § 102(e) as allegedly being anticipated by U.S. Patent No. 6,309,879. Specifically, the Examiner has alleged that the above claims are drawn to antibodies which bind to polypeptides that are at least 91%, 92%, 93%, 95% or 100% identical to SEQ ID NO:2. The Examiner further alleges that the '879 patent not only teaches a polypeptide sequence that is 99.6% identical to SEQ ID NO:2, but also antibodies binding to such polypeptide sequence.

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In response, Applicants respectfully submit that the 6,309,879 patent was the losing party to Applicants' related application USSN 09/060,939, having the same inventors and filing date as the parent application (USSN 09/292,505, U.S.P. 6,348,575) of the pending application. The U.S.P.T.O. has already determined in a prior action that Applicants are the actual inventors of the subject matter claimed in the '879 patent. A copy of the final decision from Interference 105,081 awarding all of claims 1-13 of '879 patent to Applicant's 09/060,939 application appears in the Appendix.

Applicants respectfully request reconsideration and withdrawal of the rejection of Claims 29-35, 37-45, 47-51, and 53-54 under 35 U.S.C. § 102(e)

The Rejection Under 35 U.S.C. § 103(a) (cited references)

Claims 36, 46, and 52 are rejected under 35 U.S.C. § 103(a) as being allegedly unpatentable over the '879 patent as applied to claims 29-35, 37-45, 47-51, and 53-54 above, and further in view of Berkower.

In response, Applicants response above under the 102 reference has eliminated the relevance of the '879 patent to the pending claims. Berkower does not teach, disclose or infer antibodies that bind SEQ ID NO:2.

Applicants respectfully request reconsideration and withdrawal of the rejection of Claims 36, 46 and 52 under 35 U.S.C. § 103(a).

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Patent Docket **P1405R1C1**

SUMMARY

Claims 29-54 are pending in the application. Claims 29, 39 and 49 have been amended without prejudice to later prosecution.

If in the opinion of the Examiner, a **telephone conference** would expedite the prosecution of the subject application, the Examiner is **strongly encouraged** to call the undersigned at the number indicated below.

This response/amendment is submitted with a transmittal letter. In the unlikely event that this document is separated from the transmittal letter or if fees are required, applicants petition the Commissioner to authorize charging our Deposit Account 07-0630 for any fees required or credits due and any extensions of time necessary to maintain the pendency of this application.

Applicants respectfully request that a timely Notice of Allowance be issued in this case.

Respectfully submitted,
GENENTECH, INC.

Date: March 21, 2005   By: _____

Craig G. Svoboda
Reg. No. 39,044
Telephone No. (650) 225-1489

170860

Appendix

The opinion in support of the decision being
entered today is not binding precedent of the Board.

Paper 13

Filed by: Trial Section Merits Panel   Filed
               Box Interference   4 April 2003
               Washington, D.C. 20231
               Tel: 703-308-9797
               Fax: 703-305-0942

UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE BOARD OF PATENT APPEALS AND INTERFERENCES

DAVID A. BUMCROT,

Junior Party
(Patent No. 6,309,879),

v.

FREDERIC DE SAUVAGE
and DAVID A. CARPENTER,

Senior Party
(Application No. 09/060,939).

Patent Interference 105,081 (NAGUMO)

Before SCHAFER, LANE, and NAGUMO, Administrative Patent Judges.

NAGUMO, Administrative Patent Judge.

JUDGMENT
(Pursuant to 37 CFR § 1.662(a))

Introduction

1.   On April 2, 2003, junior party Bumcroft filed Paper 12, in which it conceded priority as to Count 1, the sole count in this interference, and acknowledged that the communication would be treated as a request for adverse judgment.

Interference 105,081   Paper No. 13
Bumcrot v. De Sauvage

Order

On consideration of the forgoing, it is:

ORDERED that judgment on priority as to Count 1 is awarded

against junior party Bumcrot,

FURTHER ORDERED that Bumcrot is not entitled to a patent

containing claims 1-13 of Bumcrot's 6,309,879 patent, which

correspond to Count 1;

FURTHER ORDERED that copies of this decision be given

appropriate paper numbers and be entered in the administrative

record of Bumcrot's 6,309,879 patent and De Sauvage's 09/060,939

application.

_____)
RICHARD E. SCHAFER   )
Administrative Patent Judge   )
)   BOARD OF PATENT
_____)   APPEALS AND
SALLY GARDNER LANE   )   INTERFERENCES
Administrative Patent Judge   )
)   INTERFERENCE
_____)   TRIAL SECTION
MARK NAGUMO   )
Administrative Patent Judge   )
)

- 2 -

Interference 105,081
Bumcrot v. De Sauvage

cc (via Facsimile and first class mail):

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- 3 -

UNITED STATES PATENT AND TRADEMARK OFFICE
TRIAL DIVISION
Facsimile Transmission Cover Sheet

Date: _4-4-03_

To: _Ginger R. Dreger_
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ORGANIZATION

@Fax #: _650-324-6653_

From: _Judge Nagumo_
         NAME

BPAI @ 703-305-0942

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1/27
1/1

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1    GTTATTTCAG GCCATGGTGT TGCGCCCGAAT TAATTCCCGA ATAAGATACA TCCAGACACATG TTGATGAGTT TGGACAAACC ACAACTAGAA TGCAGTGAAA
     CAATAAAGTC CGGTACCACA ACGCGGCTTA ATTAAGGGCT AGGTCTGTAC TATTCTATGT AACTACTCAA ACCTGTTTGG TGTTGATCTT ACGTCACTTT
     (SEQ ID NO:1)

101  AAAATGCTTT ATTTGTGAAA TTTGTGATGC TATTGCTTTA TTATAAGCTG CAATAAACAA GTTGGGCCAT GGCGGCCAAG CTTCTGCAGG
     TTTTACGAAA TAAACACTTT AAACACTACG ATAACGAAAT AATATTCGAC GTTATTTGTT CAACCCGGTA CCGCCGGTTC GAAGACGTCC

201  TCGACTCTAG AGGATCCCCG GGGAATTCCG GCATGACTCG CTCCAGAGAGC TGCCCCCGAG TTACACACCC CCGCAGCACC
     AGCTGAGATC TCCTAGGGGC CCCTTAAGGC CGTACTGAGC GAGTCTCTCG ACGGGGGCTC AATGTGTGGG GGCGTCGTGG
                                     M  T  R   S  P  P   L  R  E  L   P  P  S   Y  T  P   P  R  T   A  A  P
                                  insert starts here (SEQ ID NO:2)
                         1

301  CCAGATCCTA GCTGGGAGCC TGAAGGCTCC ACTCTGGCTT CGTGCTTACT TCCAGGGCCT GCTCTTCTCT CTGGGATGCG GGATCCAGAG ACATTGTGGC
     GGTCTAGGAT CGACCCTCGG ACTTCCGAGG TGAGACCGAA GCACGAATGA AGGTCCCGGA CGAGAAGAGA GACCCTACGC CCTAGGTCTC TGTAACACCG
     Q  I  L   A  G  S  L   K  A  P   L  W  L   R  A  Y  F   Q  G  L   L  F  S   L  G  C  G   I  Q  R   H  C  G
24

401  AAAGTGCTCT TTCTGGGACT GTTGGCCTTT GGGGCCCCTG GTTAGGTCT CCGCATGGCC ATTATTGAGA CAAACTTGGA ACAGCTCTGG GTAGAAGTGG
     TTTCACGAGA AAGACCCTGA CAACCGGAAA CCCCGGGGAC GTAATCCAGA GGCGTACCGG TAATAACTCT GTTTGAACCT TGTCGAGACC CATCTTCACC
     K  V  L  F   L  G  L   L  A  F   G  A  L   A  L  G  L   R  M  A   I  I  E  T   N  L  E   Q  L  W   V  E  V  G
57

501  GCAGCCGGGT GAGCCAGGAG CTGCATTACA CCAAGGAGAA GCTGGGGGAG GAGGCTGCAT CACACCTCA GATGCTGATA ACACCCTCA GCCAGGAGGG
     CGTCGGCCCA CTCGGTCCTC GACGTAATGT GGTTCCTCTT CGACCCCCTC CTCCGACGTA GTGTGGAGT CTACGACTAT GTCTGGGCGTG CGGTCCTCCC
     S  R  V   S  Q  E   L  H  Y  T   K  E  K   L  G  E   E  A  A  Y   T  S  Q   M  L  I   Q  T  A  R   Q  E  G
91

601  AGAGAACATC CTCACACCCG AAGCACTTGG CCTCCACCTC CAGGCAGCCC TCACTGCCAG TAAAGTCCAA GTATCACTCT ATGGGAAGTC CTGGGATTTG
     TCTCTTGTAG GAGTGTGGGC TTCGTGAACC GGAGGTGGAG GTCCGTCGGG AGTGACGGTC ATTTCAGGTT CATAGTGAGA TACCCTTCAG GACCCTAAAC
     E  N  I   L  T  P  E   A  L  G   L  H  L   Q  A  A  L   T  A  S   K  V  Q   V  S  L  Y   G  K  S   W  D  L
124

701  AACAAAATCT GCTACAAGTC AGGAGTCCC CTTATTGAAA ATGGAATGAT TGAGTGGATG ATTGAGAAGC TGTTTCCGTG CGTGATCCTC ACCCCCCTCG
     TTGTTTTAGA CGATGTTCAG TCCTCAAGGG GAATAACTTT TACCTTACTA ACTCACCTAC TAACTCTTCG ACAAAGGCAC GCACTAGGAG TGGGGGGAGC
     N  K  I  C   Y  K  S   G  V  P   L  I  E  N   G  M  I   E  W  M   I  E  K  L   F  P  C   V  I  L   T  P  L  D
157

801  ACTGCTTCTG GGAGGGAGCC AAACTCCAAG GGGGCTCCGC CTACCTGCCC GGCCGCCCGG GATCCAGAGC GACCAACCTG AGCTGCTGGA
     TGACGAAGAC CCTCCCTCGG TTTGAGGTTC CCCCGAGGCG GATGGACGGG CCGGCGGGCC CTAGGTCTCG CTGGTTGGAC TCGACGACCT
     C  F  W   E  G  A   K  L  Q  G   G  S  A   Y  L  P   G  R  P  D   I  Q  W   T  N  L   D  P  E  Q   L  L  E
191
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FIG. 1A

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901  GGAGCTGGGT CCCTTGCCT  CCCTTGAGGG CTTCCGGGAG CTGCTAGACA AGGCACAGGT GGGCCAGGCC TACGTGGGGC GGCCCTGTCT GCACCCTGAT
     CCTCGACCCA GGGAAACGGA GGGAACTCCC GAAGGCCCTC GACGATCTGT TCCGTGTCCA CCCGGTCCGG ATGCACCCCG CCGGGACAGA CGTGGGACTA
224   E  L  G    P  F  A  S    L  E  G    F  R  E    L  L  D  K    A  Q  V    G  Q  A    Y  V  G  R    P  C  L    H  P  D

1001 GACTTCCACT GCCCACCTAG TGCCCCCAAC CATCACAGCA GGCAGGCTCC CAATGTGGCT CACGAGCTGA GTGGGGGCTG CCATGGCTTC TCCCACAAAT
     CTGGAGGTGA CGGGTGGATC ACGGGGGTTG GTAGTGTCGT CCGTCCGAGG GTTACACCGA GTGCTCGACT CACCCCCGAC GGTACCGAAG AGGGTGTTTA
257   D  L  H  C    P  P  S    A  P  N    H  H  S  R    Q  A  P    N  V  A    H  E  L  S    G  G  C    H  G  F    S  H  K  F

1101 TCATGCACTG GCAGGAGGAA TTGCTGCTGG GCAGAGACCC CAAGGAGAGC TGCTGAGGGC AGAGGCCCTG CAGAGCACCT TCTTGCTGAT
     AGTACGTGAC CGTCCTCCTT AACGACGACC CGTCTCTGGG GTTCCTCTCG ACGACTCCCG TCTCCGGGAC GTCTCGTGGA AGAACGACTA
291   M  H  W    Q  E  E    L  L  L  G    R  D  P    Q  G  E  L    L  R  A    E  A  L    Q  S  T    F  L  L  M

1201 GAGTCCCCGC CAGTGTACG  AGCATTTCCG GGGTGACTAT CAGACACATG ACATTGGCTG GAGTGAGGAG CCACCACCCT GGATGACATC CTGCATGCGT
     CTCAGGGGCG GTCACACATGC TCGTAAAGGC CCCACTGATA GTCTGTGTAC TGTAACCGAC CTCACTCCTC GGTGGTGGGA CCTACTGTAG GACGTACGCA
324   S  P  R    Q  L  Y  E    H  F  R    G  D  Y    Q  T  H  D    I  G  W    S  E  E    Q  A  S  T    T  L  D  D  I    L  H  A  F

1301 CGGCGCTTTG TGCAGCTGGC CCAGGAGGCC CTGCCCTGAGA ACGCTTCCCA GCAGATCCAT GCAGATCCAT ...
     GCCGCGAAAC ACGTCGACCG GGTCCTCCGG GACGGGACTCT TGCGAAGGGT CGTCTAGGTA ...
357   R  R  F  V    Q  L  A    Q  E  A    L  P  E  N    A  S  Q    I  H    A  F  S  S

1401 TCTCTGAAGT CAGTGGTGG  CGTGTGGTGG GAGGCTATCT GCCTATGCCT GTGTGACCAT GCTGCGGTGG GACTGCGCCC AGTCCCAGGG
     AGAGACTTCA GTCACCACC  GCACACCACC CTCCGATAGA CGGATACGGA CACACTGGTA CGACGCCACC CTGACGCGGG TCAGGGTCCC
391   S  E  V    S  A  A    R  V  V  G    G  Y  L    M  L  A    Y  A  C    V  T  M    L  R  W    D  C  A  Q    S  Q  G

1501 TTCCGTGGGC CTTGCCCTGGG TACTGCTGGT GGCCCTGGCG GTGGCCTGCCCAG CCCTTGGGCT CTCGGCATCA CCTTCAATGC TGCCACTACC
     AAGGCACCCG GAACGGGACCC ATGACGACCA CCGGGACCGC CACCGGACGGGTC GGGAACCCGA GAGCCGTAGT GGAAGTTACG ACGGTGATGG
424   S  V  G    L  A  G  V    L  L  V    A  L  A    V  A  S  G    L  G  L    C  A  L    G  I  T    F  N  A    A  T  T

1601 CAGGTGCTGC CTTTCTTGGC TCTGGGGATG GGCGTGGATG ACGTATTCCT GGCTCACGCC TTCACAGAGG CCCTTCCTGG GACCCCGCTT CTCCAGGAGC
     GTCCACGACG GAAAGAACCG AGACCCCTAC CCGCACCTAC TGCATAAGGA CCGAGTGCGG AAGTGTCTCC GGGAAGGACC CTGGGGCGAA GAGGTCCTCG
457   Q  V  L  P    F  L  A    L  G  I    G  V  D  D    V  F  L  A  H    A  F  T  E    A  L  P    G  T  P    L  Q  E  R

1701 GCATGGGCGA GTGTCTGCAG CGCACGGGCA CCAGTGTCGT ACTCACGTCG ATCAACAACA TGGCGGCCTT CCTCATGGCT GCCCTCGTTC CCATCCCTGC
     CGTACCCGCT CACAGACGTC GCGTGCCCGT GGTCACAGCA TGAGTGCAGC TAGTTGTTGT ACCGCCGGAA GGAGTACCGA CGGGAGCAAG GGTAGGGACG
491   M  G  E    C  L  Q  R    T  G  T    S  V  V    L  T  S    I  N  N  M    A  A  F    L  M  A    A  L  V  P    I  P  A
```

FIG. 1B

1801 GCTGGCGAGCC TTCTCCCTAC AGGCGGCCAT AGTGGTTGGC TGCACCTTTG TAGCCGTGAT GCTGTGCTTC CCAGCCATCC TCAGCCTGGA CCTACGGGGG
      CGACGCTCGG AAGAGGGATG TCCGCCGGTA TCACCAACCG ACGTGGAAAC ATCGGCACTA CGAACAGAAG GGTCGGTAGG AGTCGGGACT GGATGCCGCC

524   L R A   F S L Q   A A I   V V G   C T F V   A V M   L V F   P A I L   S L D   L R R

1901 CGCCACTGCC AGGCGCCTTGA TGTGCTCTGC GTCCCTGCTC TGCTTCTCCA GCTGGGGGAC GCTGGGGGAC GGGACAGTAC
      GCGGTGACGG TCCGCGGAACT ACACGAGACG TCGGGACGAG ACGAAGAGGT CGACCCCCTG CCCTGTCATG

557   R H C Q   R L D   V L C   F S S   P C S   A Q V   I Q I L   P Q E   L G D   G T V P

2001 CAGTGGGGCAT TGCCCACCTC ACTGCCACAG TTCAAGGCTT TACCCCACTGT GAAGCCAGCA GGTCACCACG CTGCCTCCCCC AAGCCCCACCT
      GTCACCCCGTA ACGGGTGGAG TGACGGTGTC AAGTTCCGAA ATGGGGTGACA CTTGGTCGT CCAGTGGTGCA GACGGAGGGG TTCGGGTGGA

591   V G I   A H L   T A T V   Q A F   T H C   E A S S   Q H V   V T I   L P P Q   A H L

2101 GGTCCCCCCA CCTTCTGACC CACTGGGCTC TGAGCCTCTTC AGCCCTGGAG GGTCCACACG AGGAGAAGCA
      CCACGGGGGT GGAAGACTGG GTGACCCGAG ACTCGGAGAAG TCGGGACCTC CCAGGTGTGC TCCTCGTGTTC CGTCTTCCGT

624   V P P P   S D P   L G S   E L F   S P G G   S T R   D L L   G Q E E   E T R   Q K A

2201 GCCTGCAAGT CCCTGCCCTG TGCCCGCTGG AATCTTGCCC CTATCAGTTT GCCCCGTGC ACATGCCAAG GCCATCGTGC
      CGGACGTTCA GGGACGGGAC ACGGGCGACC TTAGAACGGG GATAGTCAAA CGGGGCAACG TGTACGGTTC CGGTAGCACG

657   A C K S   L P C   A R W   N L A H   F A R   Y Q F   A P L L   L Q S   H A K   A I V L

2301 TGGTGCTCTT TGGTGTCTGA GCCTCTACGG GTGCCTGGGG GTGCTGGCCCT GACGGATGTG GCACCAAGGA
      ACCACGAGAA ACCACAGAAA CGGAGATGCC CACGGACCGG CACGTTCCTG CTGGCTACAC CGTGGTTCCT

691   V L F   G A L   L G L S   L Y G   A T L   V Q D G   L A L   T D V V   P R G   T K E

2401 GCATGCCTTC CTGAGCGCCCC AGCTCAGGTA CTTCTCCCTG TACGAGGTGG CCCTGGTGAC CCCATTCCCA ACGGCCCTC
      CGTACGGAAG GACTCGCGGG TCGAGTCCAT GAAGAGGGAC ATGCTCCACC GGGACCACTG GGGTAAGGGT TGCCGGGGAG

724   H A F   L S A Q   L R Y   F S L   Y E V A   L V T Q   G G   F D Y A   H S Q   R A L

2501 TTTGATCTGC ACCAGAGGCTT CAGTTCCCTC AAGGCCGGTGC GGCCACCCAG GCACCCCGCA CTATTACCGC AACTGGCTAC
      AAACTAGACG TGGTCCCGAA GTCAAGGGAG TTCCGGCCACG CCGGTGGGCGT CGTGGGGCGT GATAATGGCG TTGACCGATG

757   F D L H   Q R F   S S L   K A V L   P P P   A T Q   A P R T   W L H   Y Y R   N W L Q

2601 AGGGAATCCA GGCTGCCTTT GACCAGGACT GGGCTTCTGG GCGGATCACC CGCCACTCGT ACCGCAATGG CCTACAAGCT
      TCCCTTAGGT CCGACGGAAA CTGGTCCTGA CCCGAAGACC CGCCTAGTGG GCGGTGAGCA TGGCGTTACC GGATGTTCGA

791   G I Q   A A F   D Q D W   A S G   R I T   R H S Y   R N G   S E D   G A L A   Y K L

FIG. 1C

```
2701 GCTCATCCAG ACTGGAGACG CCCAGGAGCC TCTGGATTTC AGCCAGCTGA CCACAAGGAA GCTGGTGGAC AGAGAGGGAC TGATTCCACC CGAGCTCTTC
     CGAGTAGGTC TGACCTCTGC GGGTCCTCGG AGACCTAAAG TCGGTCGACT GGTGTTCCTT CGACCACCTG TCTCTCCCTG ACTAAGGTGG GCTCGAGAAG
824   L  I  Q    T  G  D  A    Q  E  P    L  D  F    S  Q  L  T    R  K    L  V  D    R  E  G  L    I  P  P    E  L  F

2801 TACATGGGGC TGACCGTGTG GGTGAGCAGT GACCCCCTGG GTCTGGCAGC CTCACAGGCC AACTTCTACC CCCCACCTCC TGAATGGCTG CACGACAAAT
     ATGTACCCCG ACTGGCACAC CCACTCGTCA CTGGGGGACC CAGACCGTCG GAGTGTCCGG TTGAAGATGG GGGGTGGAGG ACTTACCGAC GTGCTGTTTA
857   Y  M  G  L    T  V  W    V  S  S    D  P  L  G    L  A  A    S  Q  A    N  F  Y  P    P  P  P    E  W  L    H  D  K  Y

2901 ACGACACCAC GGGGGAGAAC CTTCGCATCC CGCCAGCTCA GCCCTTGGAG TTTGCCCAGT TCCCCTTCCT GCTGCGTGGC CTCCAGAGA CTGCAGACTT
     TGCTGTGGTG CCCCCTCTTG GAAGCGTAGG GCGGTCGAGT CGGGAACCTC AAACGGGTCA AGGGGAAGGA CGACGCACCG GAGGTCTCT GACGTCTGAA
891   D  T  T    G  E  N    L  R  I  P    P  A  Q    P  L  E    F  A  Q  F    P  F  L    L  R  G    L  Q  K  T    A  D  F

3001 TGTGGAGGCC ATCGAGGGGG CCCGGGCCAGC ATGGCGCAGAG CCGGGGTGCA CTGGGGTGCA GCCTACCCC AGCGGGTCCC CTGGGAACAG
     ACACCTCCGG TAGCTCCCCC GGGCCCGTCG TACCGCGTCTC GGCCCCACGT GACCCCACGT CGGATGGGG TCGCCCAGGG GACCCTTGTC
924   V  E  A    I  E  G  A    R  A  A    C  A  E    A  G  Q  A    G  V  H    A  Y  P    S  G  S  P    F  L  F    W  E  Q

3101 TATCTGGGGC TGCGGCGCTG CTTCCTGCTG GCCGTCTGCA TCCTGCTGGT GTGCACTTTC CTCGTCTGT CCTCAACCCC TGGACGGCTG
     ATAGACCCCG ACGCCGCGAC GAAGGACGAC CGGCAGACGT AGGACGACCA CACGTGAAAG GAGCAGACA GGAGTTGGGG ACCTGCCGAC
957   Y  L  G  L    R  R  C    F  L  L    A  V  C  I    L  L  V    C  T  F    L  V  C  A    L  L  L    N  P  W    T  A  G

3201 GCCTCATAGT GCTGGTCCTG CGATGATGA CAGTGGAACT CTTTGGTATC ATGGGGTTCC GCTGAGTGCC ATCCCCGTGG TGATCCTTGT
     CGGAGTATCA CGACCAGGAC GCTACTACT GTCACCTTGA GAAACCATAG TACCCCAAGG CGACTCACGG TAGGGGCACC ACTAGGAACA
991   L  I  V  L    V  L    ...  A  M  M    T  V  E  L    F  G  I    M  G  F  L    G  I  K    L  S  A    I  P  V  V    I  L  V

3301 GGCCTCTGTA GGCATTGGCG TTGAGTTCAC AGTCCACGTG GCTCTGGGCT TCCTGACCAC CAGGGGCAGC GGGCCGCCCA TGCCCTTGAG
     CCGGAGACAT CCGTAACCGC AACTCAAGTG TCAGGTGCAC CGAGACCCGA AGGACTGGTG GTCCCCGTCG CCCGGCGGGT ACGGGAACTC
1024  A  S  V    G  I  G  V    E  F  T    V  H  V    A  L  G  F    L  T  T    Q  G  S    R  N  L  R    A  A  H    A  L  E

3401 CACACATTTG CCCCCGTGAC ATCTCCACAT TGCTGGGTCT GCTCATGCTT CATTGTAAGG TACTTCTTTG
     GTGTGTAAAC GGGGGCACTG TAGAGGTGTA ACGACCCAGA CGAGTACGAA GTAACATTCC ATGAAGAAAC
1057  H  T  F  A    P  V  T    D  G  A    I  S  T  L    L  G  L    L  M  L    A  G  S  H    F  D  F    I  V  R    Y  F  F  A

3501 CGGCGCTGAC AGTGCTCACG CTCCTCCATGG CTCCTCGGGCC CCTGGGCCCG TGCTGTCCAT CCTGCCAGAGG TGATACAGAT
     GCCGCGACTG TCACGAGTGC GAGGAGGTACC GAGGAGCCCG GGACCCGGGC ACGACAGGTA GGACGGTCTCC ACTATGTCTA
1091  A  L  T    V  L  T    L  L  G  L    H  G  L    V  L  L    P  V  L    S  I    L  G  P    P  E  V    I  Q  M
```

FIG. 1D

3601 GTACAAGGAA AGCCCAGAGA TCCTGAGTCC ACCAGCTCCA CAGGGGAGCG GGGGGCATCC TCCTCCCTGC CCCAGAGCTT TGCCAGAGTG
     CATGTTCCTT TCGGGTCTCT AGGACTCAGG TGGTCGAGGT GTCCCCTCGC CCCCGTAGG AGGAGGGACG GGGTCTCGAA ACGGTCTCAC
1124 Y K E   S P E I   L S P   P A P   Q G G G   L R W   G A S   S S L P   Q S F   A R V

3701 ACTACCTCCA TGACCGTGGC CCCCCCCTGC CATCCATCCA GCCCCCTGATG AGCCCCCTG GTCCCCTGCT GCCACTAGCT
     TGATGGAGGT ACTGGCACCG GGGGGGGACG GTAGGTAGGT CGGGGGACTAC TCGGGGGAAC CAGGGGACGA CGGTGATCGA
1157 T T S M   T V A   I H P   P P L P   G A Y   I H P   A P D E   P P W   S P A   A T S S

3801 CTGGCAACCT CAGTTCCAGG GGACCCACTGG CAGCCACTGG GTGAAAGAGC AGAGACCAT GTGTGGGGCG TGTGGGGTCA CTGGGAAGCA
     GACCGTTGGA GTCAAGGTCC CCTGGGTGACC GTCGGTGACC CACTTTCTCG TCTCTGGTA CACACCCCGC ACACCCCAGT GACCCTTCGT
1191 G N L   S S R   G P G P   A T G 0

3901 CTGGGTCTGG TGTTAGACGC AGGACGGACC CCTGCTGGGGC CCTGCTGCTG CTGCATCCCC TCTCCCGACC CAGCTGTCAT GGGCCTCCCT GATATCGAAT
     GACCCAGACC ACAATCTGCG TCCTGCCTGG GGACGACGAC GACGTAGGGG AGAGGCTGG GTCGACAGTA CCCGGAGGA CTATAGCTTA
     A to C (silent)   pRK follows, this is the 5prime end of vector A

4001 TCAATCGATA GAACCGAGGT GCAGTTGGAC
     AGTTAGCTAT CTTGGCTCCA CGTCAACCTG

FIG. 1E

(SEQ ID NO: 3)

```
                        30        40        50        60        70
    905531     GCTGGGGTGCACGCCTACCNCAGCGGNTCCCCCTTCCTCTTCTGGGAACA
                :::  ::    :   ******* ****  ****************** **
    hpatched   CTGGGGCTGTCCAGTTACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCA
               3010      3020      3030      3040      3050
```

(SEQ ID NO: 4)

```
                        80        90        100       110       120
    905531     GTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGG
               ***   *  *****  **  *  ***   *  ******  *  ** **  *  **  ***
    hpatched   GTACATCGGCCTCCGCCACTGGCTGCTGCTGTTCATCAGCGTGGTGTTGG
               3060      3070      3080      3090      3100
```

```
                        130       140       150       160       170
    905531     TGTGCACTTTCCTCGTCTGTGCTCTGCTGCTCCTNAACCCCTGGACGGCT
               *****  ********  **  ***  *   *  **  ****************
    hpatched   CCTGCACATTCCTCGTGTGCGCTGTCTTCCTTCTGAACCCCTGGACGGCC
            3110      3120      3130      3140      3150
```

```
                        180       190       200       210       220
    905531     GGCCTNATAGTGCTGGTCCTGGCGATGATGACAGTGGAACTCTTTGGTAT
               **    ****  ***  **********  *******  **  **  **  **  **  **
    hpatched   GGGATCATTGTGATGGTCCTGGCGCTGATGACGGTCGAGCTGTTCGGCAT
               3160      3170      3180      3190      3200
```

```
                        230       240       250
    905531     CATGGGTTTNCTGGGCATCAAGCTGAGT
               ****   **  *  **  *******  ***
    hpatched   GATGGGCCTCATCGGAATCAAGCTCAGT
               3210      3220      3230
```

```
                        80        90        100       110       120
    905531     TCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGT
               :::     :::      *  **  *  ** *****    ****     *  **  ****
    hpatched   GCTGCTGCTGTTCATCAGCGTGGTGTTGGCC---TGCACATTCCTCGTGT
                         3090      3100      3110      3120
```

```
                        130       140       150
    905531     GCACTTTCCTCGTCTGTGCTCTGCTGCT
               **  **  **  **  *            :         :
    hpatched   GCGCTGTCTTCCTTCTGAACCCCTGGAC
            3130      3140      3150
```

FIG. 2A

(SEQ ID NO: 5) 1326258
```
        30         40         50         60         70
    GCTGGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACA
         ::: ::   :    ****** ***** ****************** **
hpatched  CTGGGGCTGTCCAGTTACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCA
        3010       3020       3030       3040       3050
```

```
             80         90        100        110        120
    1326258  GTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGG
             ***   *  ***** **  *  ***  *  ******  *  **  **  *  **  ***
hpatched  GTACATCGGCCTCCGCCACTGGCTGCTGCTGTTCATCAGCGTGGTGTTGG
             3060       3070       3080       3090       3100
```

```
             130        140        150
    1326258  TGTGCACTTTCCTCNTCTGTGCTCT
             ****  ********  **  ***  *
hpatched  CCTGCACATTCCTCGTGTGCGCTGT
          3110       3120       3130
```

```
                  90        100        110        120        130
    1326258  TCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGT
             ::   :::    * ** * ** ***** ****    * ** ****
hpatched  GCTGCTGCTGTTCATCAGCGTGGTGTTGGCC---TGCACATTCCTCGTGT
              3090       3100       3110       3120
```

```
             140        150
    1326258  GCACTTTCCTCNTCTGTGCTCT
             **  **  **  ****        :
hpatched  GCGCTGTCTTCCTTCTGAACCC
          3130       3140
```

```
              10         20         30        .40         50
    1326258  CCGGGCAGCATGCGCAGAGGCCGGCCAGGCTGGGGTGCACGCCTACCCCA
             ****** *****   ** ** * *** ****** *        :
(SEQ ID NO: 6) hpatched.RC CCGGGCGGCATG--GCGAAGCGGACCACGCTGGGGGGTGGCTCAGGGGAG
              710        720        730        740        750
```

FIG. 2B

(SEQ ID NO. 1) PTCH
(SEQ ID NO. 2) PTCH2

```
PTCH    1 MASAGNAAEPQDRGGGGSGCIGAPGRPAGGGRRRTGGLRRAAAPDRDYL
PTCH2   1 ..................MTRSPPLREL.

PTCH   51 HRPSYCDAAFALEQISKGKATGRKAPLWRAKFQRLLFKLGCYIQKNCGK
PTCH2  11 .PPSYTPP..ARTAAPQILAGSLKAPLWRAYFQGLLFSLGCGIQRHCGK

         TM1
PTCH  101 FLVGLLIFGAFAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEE
PTCH2  58 VLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEE

PTCH  151 AMFNPQLMIQTPKEEGANVLTTEALLQHLDSALQASRVHVYMYNRQWKLE
PTCH2 108 AIAYTSQMLLQTAROEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLN

PTCH  201 HLCYKSGELITETGYMDQIIEYLYPCLIITPLDCFWEGAKLQSGTAYLLG
PTCH2 158 KICYKSGVPLIIENGMIEWMIEKLFPCVLITPLDCFWEGAKLQGGSAYLPG

PTCH  251 KPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGYMDRPCLNPA
PTCH2 208 RPDIQWTNLDPEQILEELGPFA.SLEGFRELLDKAQVGQAYVGRPCLHPD

PTCH  301 DPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNS
PTCH2 257 DLHCPPSAPNHHSRQAPNVAHELLSGGCHGFSHKFMHWQEELLGGMARDP

PTCH  351 TGKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH.INWNEDKAAAILEAW
PTCH2 307 QGELLRAEALQSTELLMSPRQLYEHFRG.DYQTHDILGWSEEQASTVLQAW

         TM2
PTCH  400 QRTYVEVVHQSVAQNSTQKVLSFTTTLDDILKSFSDVSIRVASGYLLM
PTCH2 356 QRRFVQLAQEALPENASQIHAFSSTTLDDILHAFSEVSAARVVGGYLLM
```

FIG. 3A

TM3

```
PTCH  450  LAYACLTMLRWDCSKSSQGAVVAAGLGLGLCSLIIG SFNAAT
PTCH2 406  LAYACVTMLRWDCAQSQGSVGLAGVLLVALAVASGLGLCALLGT TFNAAT

                                                    TM4
PTCH  500  TQVLPFLALGVGVDDVFLLAHAFSETGQNKRIPFEDRTGECLIKRTGAS VA
PTCH2 456  TQVLPFLALGVGVDDVFLLAHAFTEALPG..TPLQERMGECLQRTGTS VV

                                  TM5
PTCH  550  LTSSNVTAFFMAALIPPALRAFSLQAAVVVFNFAMVLLFPAILSMD
PTCH2 504  LTSINNMAAFLMAALVPIPALRAFSLQAAIVGCTEVAVMLVFPAILSLD

PTCH  600  LYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHS
PTCH2 554  LRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGT........VPVG

PTCH  650  FAHETQITMQSTVQLRTEYDPHTHVVYYTTAEPRSEISVQPVTVTQDTLSC
PTCH2 593  IAH.....LTAIVQAFIHCEASSQHVVILPPQAHLVPPP....SDPLGS

PTCH  700  QSPESTSSTRDLLSQFSDSSLH..CLEPPCTKWTLSSFAEKHYAPFLLKP
PTCH2 634  ELFSPGGSTRDLLGQEETRQKAACKSLPCARWNLAHFARYQFAPLLLQS

                  TM7
PTCH  748  KAKVVVIFFLGLLGVSLYGTTRVRDGLDLTDIVPRETREYDFIAAQFKY
PTCH2 684  HAKAIVLVLFGAILGLSLVGAILVQDGLAILTDVVPRGIKEHAFLSIAQLRY

PTCH  798  FSFYNMYIVTQKA.DYPNIQHLLYDLHRSFSNVKYVMLEENKQLPKMWLH
PTCH2 734  FSLYEVALVIQGGFDYAHSQRALFDLHQRFSISLKIAVLPPPATQAPRTWLH
```

FIG. 3B

FIG. 3C

PTCH 1247 AGGP|PA|HQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPG
PTCH2 1182 PWS|PA|ATSSGNLSSRGPGPATG

PTCH 1297 RQGQQPRRDPPREGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARS

PTCH 1347 HNPRNPASTAMGSSVPGYCQPITTVTASASVTVAVHPPPVPGPGRNPRGG

PTCH 1397 LCPGYPETDHGLFEDPHVPFHVRCERRDSKVEVIELQDVECEERPRGSSS

PTCH 1447 N

FIG. 3D
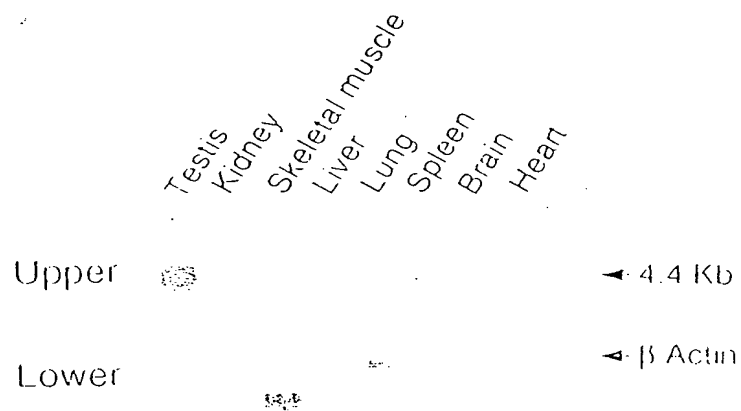
FIG. 4

FIG. 5

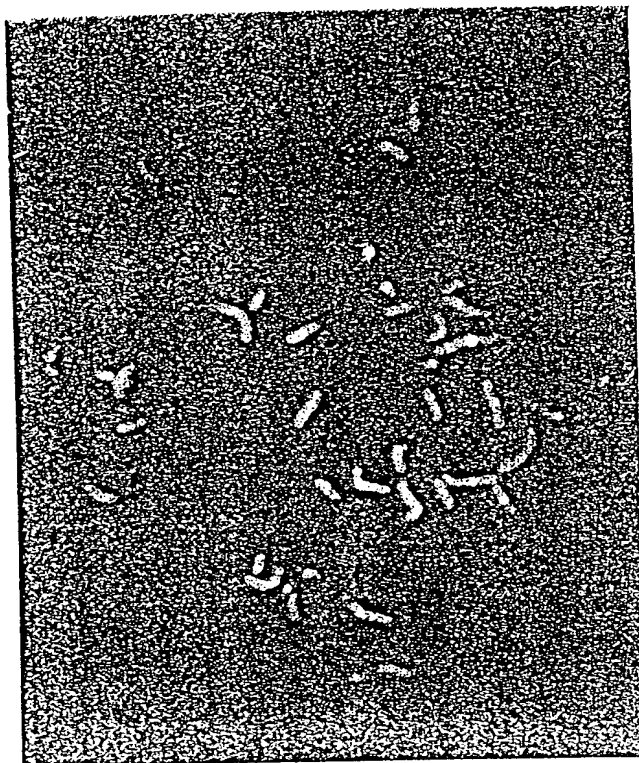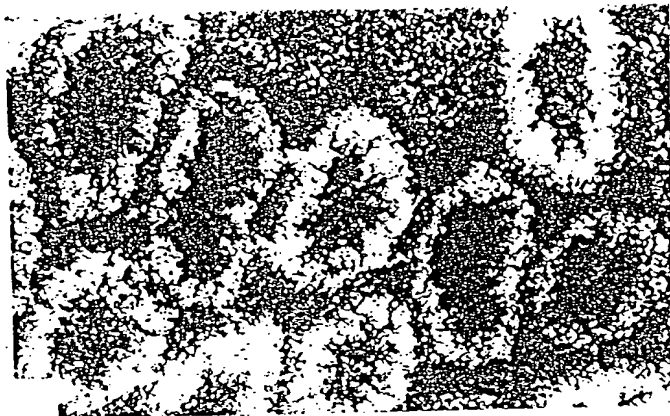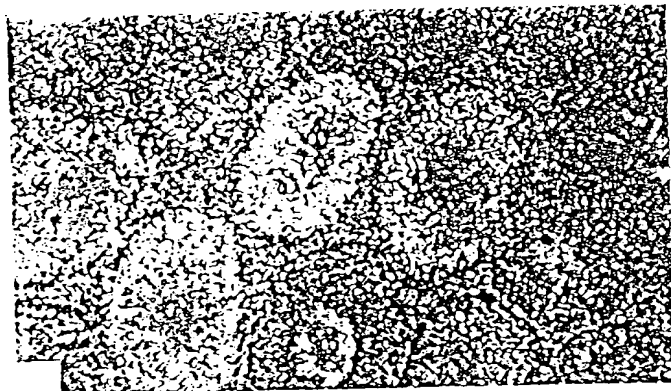FIG. 6A   FIG. 6B   FIG. 6C
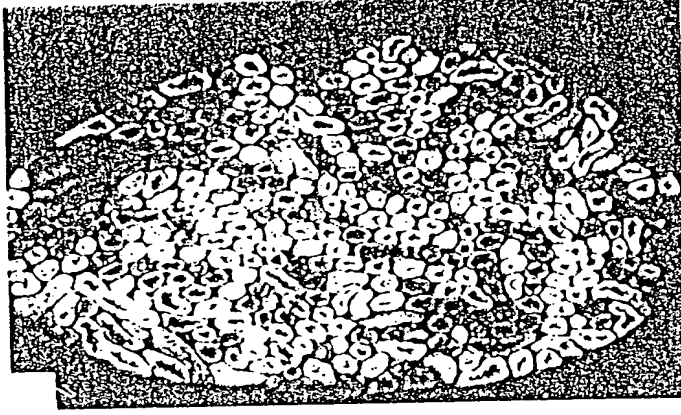
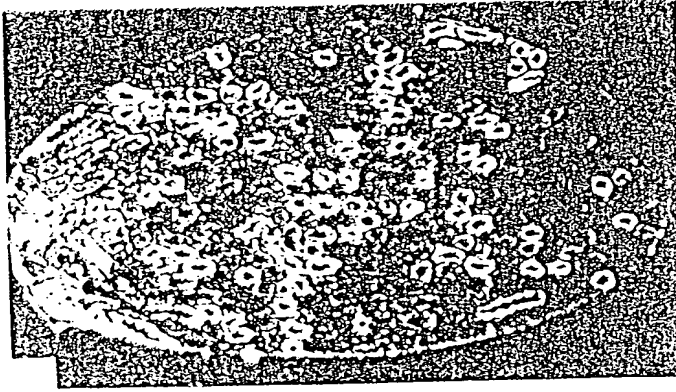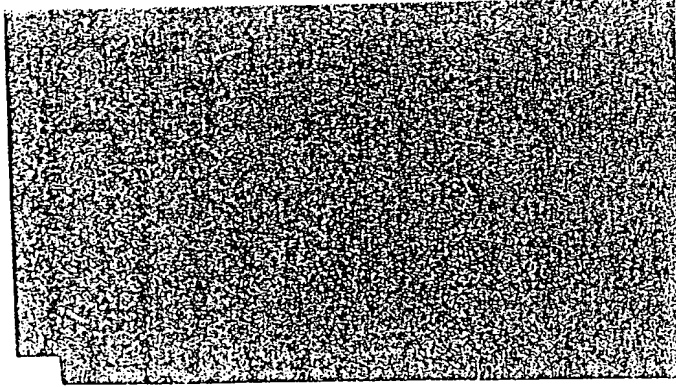FIG. 6D

FIG. 6E

FIG. 6F
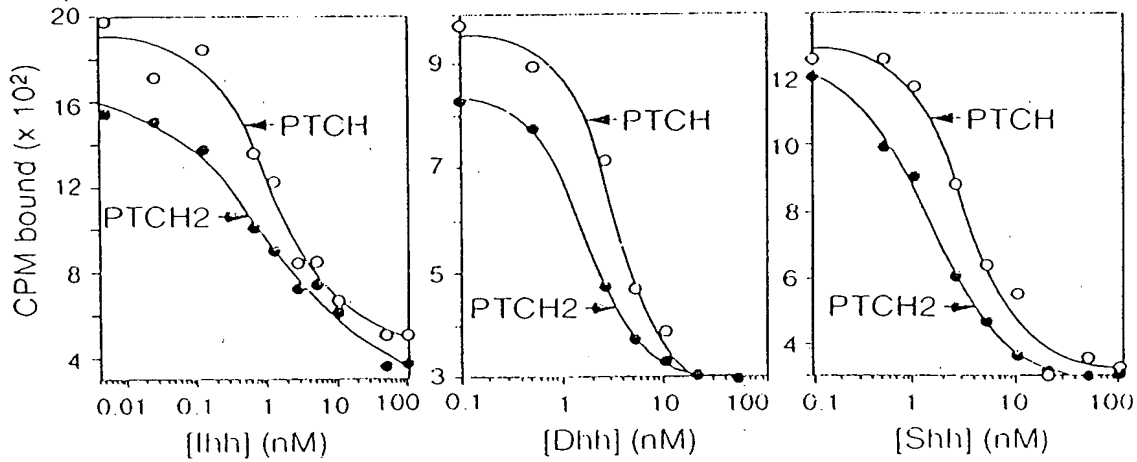
FIG. 7A
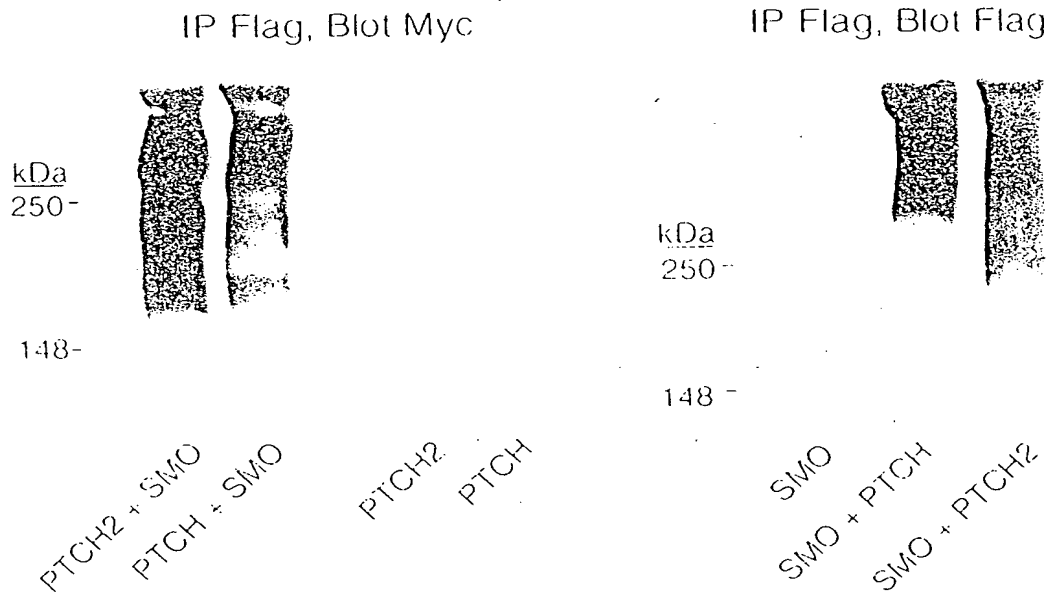
FIG. 7B

```
                10          20          30          40          50
hPtch-2    MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCG
           *  *.  .* * * * * * * * * * . .** .* * * * * . * * * * * * * * * * * * * * * *
mPatched2  MVRPLSLGELPPSYTPPARSSAPHILAGSLQAPLWLRAYFQGLLFSLGCR
~~(SEQ ID NO.7)~~ a
                10          20          30          40          50


                60          70          80          90          100
hPtch-2    IQRHCGKVLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYT
           * * . * * * * * * * * . * * * * * * * * * . * . * * * . * * * * * * * * * * * * * * * * * *
mPatched2  IQKHCGKVLFLGLVAFGALALGLRVAVIETDLEQLWVEVGSRVSQELHYT
                60          70          80          90          100


                110         120         130         140         150
hPtch-2    KEKLGEEAAYTSQMLIQTARQEGENILTPEALGLHLQAALTASKVQVSLY
           * * * * * * * * * * * * * * * * * * . * * *  * . * * * * * . * * * * * * * * * * * * * *
mPatched2  KEKLGEEAAYTSQMLIQTAHQEGGNVLTPEALDLHLQAALTASKVQVSLY
                110         120         130         140         150


                160         170         180         190         200
hPtch-2    GKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTPLDCFWEGAKLQG
           * * * * * * * * * * * * * * * * * * * * * * . * * * * * * * * * * * * * * * * * * * * * * * *
mPatched2  GKSWDLNKICYKSGVPLIENGMIERMIEKLFPCVILTPLDCFWEGAKLQG
                160         170         180         190         200


                210         220         230         240         250
hPtch-2    GSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDKAQVGQAYVGR
           * * * * * * * * * * * * * * * * * * . * * * * * * * * * * * * * * * * * * * * * * * * * * * *
mPatched2  GSAYLPGRPDIQWTNLDPQQLLEELGPFASLEGFRELLDKAQVGQAYVGR
                210         220         230         240         250


                260         270         280         290         300
hPtch-2    PCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG
           * * * . * * *  * * * * * * * . * * * * * * * * . * * * * * * * * * * * * * * * * * * * * * *
mPatched2  PCLDPDDPHCPPSAPNRHSRQAPNVAQELSGGCHGFSHKFMHWQEELLLG
                260         270         280         290         300


                310         320         330         340         350
hPtch-2    GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQAST
           *  * * *  * * . * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
mPatched2  GTARDLQGQLLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASM
                310         320         330         340         350
```

FIG. 8A

```
                 360        370        380        390        400
hPtch-2   VLQAWQRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVG
          ************************ ******************.*****..****
mPatched2 VLQAWQRRFVQLAQEALPANASQQIHAFSSTTLDDILRAFSEVSTTRVVG
                 360        370        380        390        400


                 410        420        430        440        450
hPtch-2   GYLLMLAYACVTMLRWDCAQSQGSVGLAGVLLVALAVASGLGLCALLGIT
          ****************************.*************************
mPatched2 GYLLMLAYACVTMLRWDCAQSQGAVGLAGVLLVALAVASGLGLCALLGIT
                 410        420        430        440        450


                 460        470        480         490        500
hPtch-2   FNAATTQVLPFLALGIGVDDVFLLAHAFTEALPGTPLQERMGECLQRTGT
          ***********************.******* * *.*** *******.***
mPatched2 FNAATTQVLPFLALGIGVDDIFLLAHAFTKAPPDTPLPERMGECLRSTGT
                 460        470        480         490        500


                 510        520        530        540        550
hPtch-2   SVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPAIL
          ** ***.*** **.*********************** * *********
mPatched2 SVALTSVNNMVAFFMAALVPIPALRAFSLQAAIVVGCNFAAVMLVFPAIL
                 510        520        530        540        550


                 560        570        580        590        600
hPtch-2   SLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV
          ******* ********************.******* .*************
mPatched2 SLDLRRRHRQRLDVLCCFSSPCSAQVIQMLPQELGDRAVPVGIAHLTATV
                 560        570        580        590        600


                 610        620        630        640        650
hPtch-2   QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEE
          *******************..*.*******.*********.***
mPatched2 QAFTHCEASSQHVVTILPPQAHLLSPASDPLGSELYSPGGSTRDLLSQEE
                 610        620        630        640        650


                 660        670        680        690        700
hPtch-2   ETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLS
          *   .***..* **.* *****************..***.**.*******
mPatched2 GTGPQAACRPLLCAHWTLAHFARYQFAPLLLQTRAKALVLLFFGALLGLS
                 660        670        680        690        700
```

FIG. 8B

~~1/19~~

```
              710        720        730        740        750
hPtch-2    LYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYA
           * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
mPatched2  LYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYA
              710        720        730        740        750


              760        770        780        790        800
hPtch-2    HSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDW
           * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * . * * * * * * * * * * * *
mPatched2  HSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRSWLQGIQAAFDQDW
              760        770        780        790        800


              810        820        830        840        850
hPtch-2    ASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLTTRKLVDREGL
           * * * * * *   * * * * * * * * * * * * * * * * * * * . * * * * * * * * * * * * * * * * * * . * * *
mPatched2  ASGRITCHSYRNGSEDGALAYKLLIQTGNAQEPLDFSQLTTRKLVDKEGL
              810        820        830        840        850


              860        870        880        890        900
hPtch-2    IPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP
           * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
mPatched2  IPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP
              860        870        880        890        900


              910        920        930        940        950
hPtch-2    PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSP
           . * * * * * * * * * * * . * * * * * * * * * * * * * * * * * * . * * * * * * * * * * * * * * *
mPatched2  AAQPLEFAQFPFLLHGLQKTADFVEAIEGARAACTEAGQAGVHAYPSGSP
              910        920        930        940        950


              960        970        980        990        1000
hPtch-2    FLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMT
           * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * . * * * * * * * * * * * * * * *
mPatched2  FLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLSPWTAGLIVLVLAMMT
              960        970        980        990        1000


              1010       1020       1030       1040       1050
hPtch-2    VELFGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLR
           * * * * * * * * * * * * * * * * * * * * * * * . * * * * * * * * * * * * * * * * * . * * * * * *
mPatched2  VELFGIMGFLGIKLSAIPVVILVASIGIGVEFTVHVALGFLTSHGSRNLR
              1010       1020       1030       1040       1050
```

FIG. 8C

```
                1060        1070        1080        1090        1100
hPtch-2     AAHALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGL
            ** ***.********.**********.****.****  *********
mPatched2   AASALEQTFAPVTDGAVSTLLGLLMLAGSNFDFIIRYFFVVLTVLTLLGL
                1060        1070        1080        1090        1100


                1110        1120        1130        1140        1150
hPtch-2     LHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGGLRWGASSSLP
            ****.**********.*.*.*****. *...*** *****. ...**
mPatched2   LHGLLLLPVLLSILGPPPQVVQVYKESPQTLNSAAPQRGGLRWDRPPTLP
                1110        1120        1130        1140        1150


                1160        1170        1180        1190        1200
hPtch-2     QSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP
            ************.********.***..**
mPatched2   QSFARVTTSMTVALHPPPLPGAYVHPASEEPT
                1160        1170        1180


hPtch-2     ATG
```
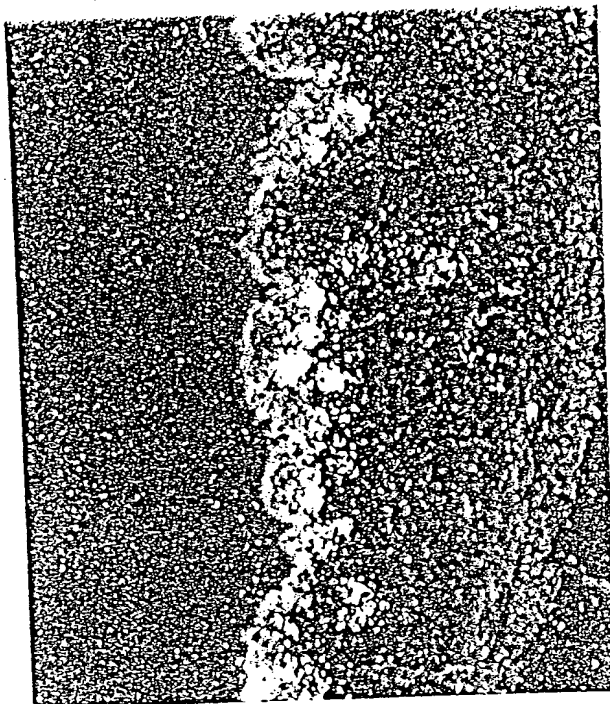
FIG. 8D

PTCH2   PTCH

FIG. 9

consensus sequence of human perched 2 cDNA clone
Length 1001 bp

(SEQ ID NO:6)

```
  1 CCCACGCGTC CGGGAGAAGC TGGGGGAGGA GGCTGCATAC ACCTCTCAGA TGCTGATACA GACCGCCACGC CAGGAGGGAG AGAACATCCT CACACCCGAA
    GGGTGCGCAG GCCCCTCTTCG ACCCCCTCCT CCGACGTATG TGGAGAGTCT ACGACTATGT CTGGCGGTGCG GTCCTCCCTC TCTTGTAGGA GTGTGGGCTT

101 GCACTTGGCC TCCACTCCA GGCAGCCCTC ACTGCCAGTA AGTCCAAGT ATCACTCTAT GGGAAGTCCT GGGATTGAA CAAAATCTGC TACAAGTCAG
    CGTGAACCGG AGGTGGAGGT CCGTCGGGAG TGACGGTCAT TTCAGGTTCA TAGTGAGATA CCCTTCAGGA CCCTAAACTT GTTTTGAGACG ATGTTCAGTC

201 GAGTTCCCT TATTGAAAAT GGAATGATTG AGCGGGATGAT TGAGAAGCTG TTTCCGTGCG CCCCCTCGAC TGCTTCTGGG AGGGAGCCAA TCCCTCGGTT
    CTCAAGGGGA ATAACTTTTA CCTTACTAAC TCGCCTACTA ACTCTTCGAC AAAGGCACGC ACTAGGAGTG GGGGAGCTG ACGAAGACCC

301 ACTCCAAGGG GGCTCCGCCT ACCTGCCGCT CCCAATGTGG CTCACGAGCT GAGTGGGGGC TCTCCCACAA ATTCATGCAC TGGCAGGAGG
    TGAGGTTCCC CCGAGGCGGA TGGACGGCGA GGGTTACACC GAGTGCTCGA CTCACCCCCG ACGGTACGGA AGAGGGTGTT TAAGTACGTG ACCGTCCTCC

401 AATTGCTGCT GGGAGGCATG GCCAGAGACC CCCAAGGAGA GCTGCTGAGG GCAGAGCCC TGCAGAGCAC CTTCTTGCTG ATGAGTCCCC GCCAGCTGTA
    TTAACGACGA CCCTCCGTAC CGGTCTCTGG GGGTTCCTCT CGACGACTCC CGTCTCCGGG ACGTCTCGTG GAAGAACGAC TACTCAGGGG CGGTCGACAT

501 CGAGCATTTC CGGGGTGACT ATCAGACACA TGACATTGGC TGGAGTGAGG AGCAGGCCAG CACAGTGCTA CAAGCCTGGC AGCGGGCGCTT TGTGCAGTC
    GCTCGTAAAG GCCCCACTGA TAGTCTGTGT ACTGTAACCG ACCTCACTCC TCGTCCGGTC GTGTCACGAT GTTCGGACCG TCGCCGCGAA ACACGTCCAG

601 GGTATGGACA AGGACAGGGG GGTGCCCTGA GGCCATTCCC TCCTCCTATC CACCCTGTTT CTCCAGCTGG CCCAGGAGGC CCTGCCTGAG
    CCATACCTGT TCCTGTCCCC CCACGGGACT CCGGTAAGGG AGGAGGACGG GTGGGACAAA GAGGTCGACC GGGTCCTCCG GGACGGACTC

701 AACGCTTCCC AGCAGATCCA TGCCCTTCTCC TCCACCACCC TGGATGACAT CCTGCATGCG TTCTCTGAAG TCAGTGCTGC CGTGTGGTG GGAGGCTATC
    TTGCGAAGGG TCGTCTAGGT ACGGAAGAGG AGGTGGTGGG ACCTACTGTA GGACGTACGC AAGAGACTTC AGTCACGACG GCACACCAC CCTCCGATAG

801 TGCTCATGGT GGTCTTGCA CCTGGCACCT TGCCCCCACC CCAGTGCCCA CCCTGGGGAG CCCCTGAGAC TGCCCTTTCC CCCCACAGCT
    ACGAGTACCA CCCAGAACGT GGACCGTGGA ACGGGGGGTGG GGTCACGGGT GGTGGAGGTT GGGACTCTG ACGGGAAAGG GGGGTGTCGA
```

FIG. 10A

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 901  GGCCTATGCC TGTGTGACCA TGCTGCGGTG GGACTGCGCC CAGTCCCTGG GTACTGCTGG CCTGCCGGGG GTGGCCTCA
      CCGGATACGG ACACACTGGT ACGACGCCAC CCTGACGCGG GTCAGGGACC CATGACGACC GGAACGGGCC ACCAGGGAGT

1001  GGCCTTGGGC TCTGTGCCCT GCTCGGCATC ACCTTCAATG CTGCCACTAC CCAGGTACGC GGGCAGACTC AGTGCCAGTC ACCAGGCTTC
      CCGGAACCCG AGACACGGGA CGAGCCGTAG TGGAAGTTAC GACGGTGATG GGTCCATGCG CCCGTCTGAG TCACGGTCAG TGGTCCGAAG

1101  ACGGGTCCTC AGCTGCCCGC TCCTCTGCCC TGCCCTTCTT GACTCTGGGA ATGACGTATT CCTGCTGCGG CATGCCTTCA
      TGCCCAGGAG TCGACGGGCG AGGAGACGGG ACGGGAAGAA CTGAGACCCT TACTGCATAA GGACGACGGC GTACGGAAGT

1201  CAGAGGCTCT GCCTGGCACC CCTCTCCAGG TGGGGCCTTG TCCCCCCAGG GCAGCTCAGC TTACTGGTTA AGAGCCTCTT GGTTCAAGTG
      GTCTCCGAGA CGGACCGTGG GGAGAGGTCC ACCCCGGAAC AGGGGGGTCC CGTCGAGTCG AATGACCAAT TCTCGGAGAA CCAAGTTCAC

1301  ACCTTGGGCT GCTAATGAAC CTCGGTGCCT CTTGTCCCCA TGTGTAAACA GGGGAAATAA TAGTGCTGTG TCCTAAGGGT TATTGTTTGG ATCAGTGAAG
      TGGAACCCGA CGATTACTTG GAGCCACGGA GAACAGGGGT ACACATTTGT CCCCTTTATT ATCACGACAC AGGATTCCCA ATAACAAACC TAGTCACTTC

1401  TAACTCAAGT TGAATGCTTA GAACAGCCCA TCATACGTAC ATGGTACCCA ATAAATGCTA GCCACTGTGT TATGACTGCC ACCCAAGTT
      ATTGAGTTCA ACTTACGAAT CTTGTCGGGT AGTATGCATG TACCATGGGT TATTTACGAT CGGTGACACA ATACTGACGG TGGGGTTCAA

1501  CCTGAGCCTC CCCTTCACTC CACTTTGACA CGGCCCCTCC CTTGTGACCT GAGGGCCAGT TCCTGGCAGG AGGCGCATGG CGAGTGTCTG
      GGACTCGGAG GGGAAGTGAG GTGAAACTGT GCCGGGGAGG GAACACTGGA CTCCCGTCCA AGGACCGTCC TCCGCGTACC GCTCACAGAC

1601  CCTGAGCCTC CCCTTCACTC CCCAGTTCCA TCCATCAACA ACATGGCCGC CTTCCTCATG GCTGCCCTCG TTCCCATCCC TGGCCTGCGA GCCTTCTCCC
      GGACTCGGAG GGGAAGTGAG AGGTCAGGGT AGGTAGTTGT TGTACCGGCG GAAGGAGTAC CGACGGGAGC AAGGGTAGGG ACGGGACGCT CGGAAGAGGG

1701  TACAGCCTGG ACCTACGGCG GGGCCACTGC CAGGCGCCTG ATGTGCTCTG CTGCTTCTCC AGTACTCTCC CCCTTCCTC CCGTGACCCA
      ATGTCGGACC TGGATGCCGC CCCGGTGACG GTCCGCGGAC TACACGAGAC GACGAAGAGG GGATGAGAGG GGGAAGGAG GGCACTGGGT

1801  CGCCAGCCTG TCCCCTCACC AGCATTTCAA GGCACAGACC TGTCATCCAC TCTCTACCTC TTCCAGTCCC AGGTGATTCA GATCCTGCCC
      GCGGTCGGAC AGGGGAGTGG TCGTAAAGTT CCGTGTCTGG ACAGTAGGTG AGAGATGGAG AAGGTCAGGG TCCACTAAGT CTAGGACGGG

1901  CAGGAGCTGG GGGACGGGAC AGTACCAGTG GGCATTGCCC ACCTCACTGC CACAGTTCAA GCCTTTACCC ACTGTGAAGC CAGCAGCCAG CATGTGGTCA
      GTCCTCGACC CCCTGCCCTG TCATGGTCAC CCGTAACGGG TGGAGTGACG GTGTCAAGTT CGGAAATGGG TGACACTTCG GTCGTCGGTC GTACACCAGT

2001  CCATCCTGCC TCCCCAAGCC CCCCACCTTC TGACCACTGG GGCTCTGAGC TCTTCAGCCC TGGAGGGTCC ACACGGGACC TTCTAGGCCA
      GGTAGGACGG AGGGGTTCGG GGGGTGGAAG ACTGGTGACC CCGAGACTCG AGAAGTCGGG ACCTCCCAGG TGTGCCCTGG AAGATCCGGT
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FIG. 10B

2101 GGAGGAGGAG ACAAGGCAGA AGGCAGCCTG CAAGTCCCTG CCCTGTGCCC GCTGGAATCT TGCCCATTTC GCCCGCTATC AGTTTGCCCC GTTGCTGCTC
     CCTCCTCCTC TGTTCCGTCT TCCGTCGGAC GTTCAGGGAC GGGACACGGG CGACCTTAGA ACGGGTAAAG CGGGCGATAG TCAAACGGGG CAACGACGAG

2201 CAGTCACATG CCAAGGCCAT CGTGCTGGTG CTCTTCTGGG CTCTTCGGTG CCTGAGCCTC TACGGAGCCA CCTTGGTGCA AGACGGCCTG GCCCTGACGG
     GTCAGTGTAC GGTTCCGGTA GCACGACCAC GAGAAACCAC GAGAAGCCC GGACTCGGAG ATGCCTCGGT GGAACCACGT TCTGCCGGAC CGGGACTGCC

2301 ATGTGGTGCC TCGGGGCACC AAGGAGCATG CCTTCCTGAG CGCCCAGCTC AGTAGTTCT CCCTGTACGA GGTGGCCCTG GTGACCCAGG GTGGCTTTGA
     TACACCACGG AGCCCCGTGG TTCCTCGTAC GGAAGGACTC GCGGGTCGAG TCCATGAAGA GGGACATGCT CCACCGGGAC CACTGGGTCC CACCGAAACT

2401 CTACGCCCAC TCCCAAGCGG CCCTCTTTGA TCTGCACCAG CGCTTCAGTT CCCTTCAAGGC GGTGCTGCCC CCCAGGCACC CCGCCACCTGG
     GATGCGGGTG AGGGTTCGGC GGGAGAAACT AGACGTGGTC GCGAAGTCAA GGGAGTTCCG CCACGACGGG GGTGCCGGT GGCGGTGGACC

2501 CTGCCACTATT ACCGCCAACTG GCTACAGGGA ATCCAGGCTG CCTTTGACCA GGACTGGGCT TCACCCGCCA CTCGTACCGC AATGGCTCTG
     GACGTGATAA TGGCGTTGAC CGATGCCCCT TAGGTCCCCT CGGAAACTGGT CCTGACCCGA AGTGGGCGGT GAGCATGGCG TTACCGAGAC

2601 AGGATGGGGC CCTGGCCTAC AAGCTGCTCA TCCAGACTGG ATTTCAGCCA GAGCCTCTGG GGTTGGGAGA GGGCTGGAGG GGTCCACTAG
     TCCTACCCCG GGACCGGATG TTCGACGAGT AGGTCTGACC TAAAGTCGGT CTCGGAGACC CCAACCCTCT CCCGACCTCC CCAGGTGATC

2701 TACAGGGGGCT GCAGGCCTCC TGGGGCCCAGG CCTTCAGCCC TCTCTGCCTC TGCAGCTGAC CACAAGGAAG CTGGTGGACA GAGAGGGACT GATTCCACCC
     ATGTCCCCGA CGTCCGGAGG ACCCCGGGTCC GGAAGTCGGG AGAGACGGAG ACGTCGACTG GTGTTCCTTC GACCACCTGT CTCTCCCTGA CTAAGGTGGG

2801 GAGCTCTTCT ACATGGGGCT GACCGTGTGG GTGAGCAGTG ACCCCCTGGG TCTGGCCAGCCA ACTTCTACCC CCCACCTCCT GAATGGCTGC
     CTCGAGAAGA TGTACCCCGA CTGGCACACC CACTCGTCAC TGGGGGACCC AGACCGTCGG AGTGTCCGGT TGAAGATGGG CTTACCGACG

2901 ACGACAAATA CGACACCACG GGGGAGAAACC TTCGCAGTGA GTCTTGGGGG GAGCTCGGCA AGAGCCTCAG CCTCGCCCAC ACAAGCCCTG AGCCTGAGGC
     TGCTGTTTAT GCTGTGGTGC CCCCTCTTGG AAGCGTCACT CAGAACCCCC CTCGAGCCGT TCTCGGAGTC GGAGCGGGTG TGTTCGGGAC TCGGACTCCG

3001 CCTGCCCACT CTGCCCCGTG CTCACCGCGCC TGTCCCTCCC CCTCCACAGT CCCGCCCAGCT CAGCCCCTTGG AGTTTGCCCA
     GGACGGGGTGA GACGGGGCAC GAGTGGCGGG ACAGGGGAGG GGAGAAGAGG GGGCGGGTCGA GTCGGGGTGTCA TCAAACGGGT

FIG. 10C

3101 GTTCCCCTTC CTGCTGCGTG GCCTCCAGAA GACTGCAGAC TTTGTGGAGG CCATCGAGGG GGCCCGGGCA GCATGGCGCA AGGCCGGCCA GGCTGGGGTG
     CAAGGGGAAG GACGACGCAC CGGAGGTCTT CTGACGTCTG AAACACCTCC GGTAGCTCCC CCGGGCCCGT TCCGGCCGGT CCGACCCCAC

3201 CACGCCTACC CCAGCGGCTC CCCCTTCCTC TTCTGGGAAC AGTATCTGGG CCTGCGGCGC TGCTTCCTGC TGGCCGTCTG CATCCTGCTG GTGTGCACTT
     GTGCGGGATGG GGTCGCCGAG GGGGAAGGAG TCATAGACCC ACGGCCGCGG GACGCCGCG GTAGGACGAC CACACGTGAA

3301 TCCTCTGCTG TGCTCTGCTG CTCCTCAACC CCTGGACGGC TGGCCTCATA GTGAGTGCTT GCAGGAGTGG GGACAGAGAC ACCCCACCCT TCCCTGCCCA
     AGGAGCAGAC ACGAGACGAC GAGGAGTTGG GGACCTGCCG CGTCCTCACC CCTGTCTCTG TGGGGTGGGA AGGGACGGGT

3401 GCCTGTCATC CCTCCTGCCA GGAGCCCTCT GTGAGCCCTG TCTCCCTCAG GTGCTGGTCC TGGCCGATGAT GACAGTGGAA CTCTTTGGTA TCATGGGTTT
     CGGACAGTAG GGAGGACGGT CCTCGGGAGA CACTCGGGAC AGAGGGAGTC CACGACCAGG ACCGCTACTA CTGTCACCTT GAGAAACCAT AGTACCCAAA

3501 CCTGGGCATC AAGCTGAGTG CCATCCCCGT GGTGATCCTT GTGGCCTCTG TAGGCATTGG CGTTGAGTTC ACAGTCCACG TGGCTCTGGT GAGCACGGGC
     GGACCCGTAG TTCGACTCAC GGTAGGGGCA CCACTAGGAA CACCGGAGAC ATCCGTAACC GCAACTCAAG TGTCAGGTGC ACCGAGACCA CTCGTGCCCG

3601 ACCCCGGGGA GGGACCAATC AGCTGATTCA GTATTCAACA CATATTGTTC AAGCCCCTAC TATGTGCTAG GTACTATTTA AGAATTTGGG CTGGGTGGAC
     TGGGGCCCCT CCCTGGTTAG TCGACTAAGT CATAAGTTGT GTATAACAAG TTCGGGGATG ATACACGATC TCTTAAACCC GACCCACCTG

3701 GTGGTGGCTC ATTCCTGTAA TCCCAGCACT TTGGGAGGCC GAGGCGGGTG GATCACCTGA GGTCGGGAGT TCGAAACCAG CCTGGCCAAC ATGGTGAAAC
     CACCACCGAG TAAGGACATT AGGGTCGTGA AACCCTCCGG CTCCGCCCAC CTAGTGGACT AGCTTTGGTC GGACCGGTTG TACCACTTTG

3801 CCTGTCTTTA CTAAAAATAC AAAAAATTAG CCAGGCGTGG TGGCACATGC CAGTAGTCCC AGCTACTTTG GAGGCTGAGG CAGAATTGCT TGAACCTGGG
     GGACAGAAAT GATTTTTATG TTTTTTAATC GGTCCGCACC ACCGTGTACG GTCATCAGGG TCGATGAAAC CTCCGACTCC GTCTTAACGA ACTTGGACCC

3901 AGGCGGAAGGT TGCAGTGAGC TGAGATCGTG CCATTGCACT CCAGCCTGGG CAACAAGAGT GCAACTCTCC GTCTCAAAAA AAAAAAAAA AAGGGCGGCC
     TCCGCTTCCA ACGTCACTCG ACTCTAGCAC GGTAACGTGA GGTGTTCTCA CGTTGAGAGG CAGAGTTTTT TTTTTTTTT TTCCCGCCGG

4001 GCGA
     CGCT

FIG. 10D

Clone 16.1 human patched 2
length 2082 bp

(SEQ ID NO:?)

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  1 TTCCGGCATG ACTCGATCGC CGCCCCTCAG AGAGCTGCCC CCGAGTTACA CACCCCCAGC TCGAACCGCA GCACCCCAGA TCCTAGCTGG GAGCCTGAAG
    AAGGCCGTAC TGAGCTAGCG GCGGGGGAGTC TCTCGACGG GGCTCAATGT GTGGGGGTCG AGCTTGGCGT CGTTGGGGTCT AGGATCGACC CTCGGACTTC

101 GCTCCACTCT GGCTTCGTGC TTACTTCCAG GGCCTGCTCT TCTCTCTGGG ATGCGGGATC CAGAGACATT GTGGCAAAGT GCTCGTTCTG GGACTGTTGG
    CGAGGTGAGA CCGAAGCACG AATGAAGGTC CCGGACGAGA AGAGAGACCC TACGCCCTAG GTCTCTGTAA CACCGTTTCA CGAGAAAGAC CCTGACAACC

201 CCTTTGGGGC CCTGGCATTA GGTCTCCGCA TGGCCATTAT TGAGACAAAC TCTGGGTAGA AGTGGGCAGC CGGGTGAGCC AGGAGCTGCA
    GGAAACCCCG GGACCGTAAT CCAGAGGCGT ACCGGTAATA ACTCTGTTTG AACCCATCT TCACCCGTCG GCCCACTCGG TCCTCGACGT

301 TTACACCAAG GAGAAGCTGG GGGAGGAGGC TGCATACACG TCTCAGATGC TGATACAGAC CGCACGCCAG ACATCCTCAC ACCCGAAGCA
    AATGTGGTTC CTCTTCGACC CCCTCCTCCG ACGTATGTGC AGAGTCTACG GCGTGCGGTC CTCCCTCTCT TGTAGGAGTG TGGGCTTCGT

401 CTTGGCCTCC ACCTCCAGGC AGCCCTCACT GCCAGTAAAG TCCAAGTATC ACTTCTATGGG ATTTGAACAA AATCTGCTAC AAGTCAGGAG
    GAACCGGAGG TGGAGGTCCG TCGGGAGTGA CGGTCATTTC AGGTTCATAG TGAGATACCC TAAACTTGTT TTAGACGATG TTCAGTCCTC

501 TTCCCCTTAT TGAAAAATGGA ATGATTGAGT GGATGATTGA GAAGCTGTTT CCGTCGCTGA TCCTCACCCC CCTCGACTGC TTCTGGGAGG GAGCCAAACT
    AAGGGGAATA ACTTTTACCT TACTAACTCA CCTACTAACT CTTCGACAAA GGCACGCACT AGGAGTGGGG GGAGCTGACG AAGACCCTCC CTCGGTTTGA

601 CCAAGGGGGC TCCGCCTACC TGCCCGGCGG CCCGGATATC CAGCTGGACCA ACCTGGATCC AGAGCAGCTG CTGGAGGAGC TGGGTCCCTT TGCCTCCCTT
    GGTTCCCCCG AGGCGGATGG ACGGGCCGCC GGGCCTATAG GTCACCTGGT TGGACCTAGG TCTCGTCGAC GACCTCCTCG ACCCAGGGAA ACGGAGGGAA

701 GAGGGCTTCC GGGAGCTGCT AGACAAGGCA CAGGTGGCGCC AGCCTACAGT GGGGCGGGCC TGTCTGCACC CTGATGACCT CCACTGCCCA CCTAGTGCCC
    CTCCCGAAGG CCCTCGACGA TCTGTTCCGT GTCCACCCGG TCCGGATGCA CCCCGCCCGG GACAGACGTGG GACTACTGGA GGTGACGGGT GGATCACGGC

801 CCAACCATCA CAGCAGGCAG GCTCCCAATG TGGCTCACGA GCTGAGTGGG GGCTGCCATG GCTTCTCCCA CAAATTCATG AGGAATTGCT
    GGTTGGTAGT GTCGTCCGTC CGAGGGTTAC ACCGAGTGCT CGACTCACCC CCGACGGTAC GTTTAAGTAC TCCTTAACGA

901 GCTGGGGAGGC ATGGCCAGAG ACCCCCCAAGG AGAGCTGCTG AGGGCAGAGG CCCTGCAGAG CACCTTCTTG CTGATGAGTC CCCGCCAGCT GTACGAGCAT
    CGACCCTCCG TACCGGTCTC TGGGGGTTCC TCTCGACGAC TCCCGTCTCC GGGACTGTCTC GTGGAAGAAC GACTACTCAG GGGCGGTCGA CATGCTCGTA
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FIG. 11A

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1001 TTCGGGGGTG ACTATCAGAC ACATGACATT GGCTGGAGTG AGGAGCAGGC CAGCACAGTG CTACAAGCCT GGCAGCGGCG CTTTGTGCAG CTGGCCCAGG
     AAGGCCCCAC TGATAGTCTG TGTACTGTAA CCGACCTCAC TCCTCGTCCG GTCGTGTCAC CGTCGCCGCG GAAACACGTC GACCGGGTCC

1101 AGGCCCTGCC TGAGAACGCT TCCAGCAGA TCCATGCCTT CTCCTCCACC ACCCTGGATA ACATCCTGCA TGCGTTCTCT GAAGTCAGTG CTGCCCGTGT
     TCCGGGACGG ACTCTTGCGA AGGGTCGTCT AGGTACGGAA GAGGAGGTGG TGGGACCTAT TGTAGGACGT ACGCAAGAGA CTTCAGTCAC GACGGGCACA

1201 GGTGGGAGGC TATCTGCTCA TGCCTGGCCTA ACCATGCTGC GGTGGGACTG CGCCCAGTCC CAGGGTTCCG TGGGCCTTGC CGGGGTACTG
     CCACCCTCCG ATAGACGAGT ACGACCGGAT TGGTACGACG CCACCCTGAC GCGGGTCAGG GTCCCAAGGC ACCCGGAACG GCCCCATGAC

1301 CTGGTGGCCC TGGGGGTGGC CTCAGGCCTT GGGCTCTGTG CCCTGCTCGG CATCACCTTC AATGCTGCCA CTACCCAGGT GCTGCCCTTC TTGGCTCTGG
     GACCACCGGG ACCGCCACCG GAGTCCGGAA CCCGAGACAC GGGACGAGCC GTAGTGGAAG TTACGACGGT GATGGGTCCA CGACGGGAAG AACCGAGACC

1401 GAATCGGCGT GGATGACGTA TTCCTGCTGG CGCATGCCTT CACAGAGGCT CTGCCTGGCA CCCCCTCTCCA GGAGCGGCATG GGCGAGTGTC TGCAGGCGCAC
     CTTAGCCGCA CCTACTGCAT AAGGACGACC GCGTACGGAA GTGTCTCCGA GACGGACCGT GGGGAGAGGT CCGCGTAC CGCTCACAG ACGTCGCGTG

1501 GGGCACCAGT GTCGTACTCA CATCCATCAA CAACATGGCC GCCTTCCTCA TGGCTGCCCT CGTTCCCATC CCTGCGCTGC GAGCCTTCTC CTTACAGCCA
     CCCGTGGTCA CAGCCATGAGT GTAGGTAGTT GTTGTACCGG CGGAAGGAGT ACCGACGGGA GCAAGGGTAG GGACGCGACG CTCGGAAGAG GAATGTCGGT

1601 TCCTCAGCCT GGACCTACGG CGGGCGCCACT GCCAGCGCCT TGATGTGCTC TGCTGCTTCT CCAGTCCCTG CTCTGCTCAG GTGATTCAGA TCCTGCCCCA
     AGGAGTCGGA CCTGGATGCC GCCCGCGGTGA CGGTCGCGGA ACTACACGAG AGGACGAAGA GGTCAGGGAC GAGACGAGTC CACTAAGTCT AGGACGGGGT

1701 GGAGCTGGGG GACGGGACAG TACCAGTGGG CATTGCCCAC CTCACTGCCA CAGTTCAAGC TGTGAAGCCA GCAGCCAGCA TGTGGTCACC
     CCTCGACCCC CTGCCCTGTC ATGGTCACCC GTAACGGGTG GAGTGACGGT GTCAAGTTCG ACACTTCGGT CGTCGGTCGT ACACCAGTGG

1801 ATCCTGCCTC CCCAAGCCCA CCTGGTGCCC CCACCTTCTG ACCCACTGGG CTCTGAGCTC TTCAGCCCTG GAGGGTCCAC ACGGGACCTT CTAGGCCAGG
     TAGGACGGAG GGGTTCGGGT GGACCACGGG GGTGGAAGAC TGGGTGACCC GAGACTCGAG AAGTCGGGAC CTCCCAGGTG TGCCCTGGAA GATCCGGTCC

1901 AGGAGGAGAC AAGGCAGAAG GCAGCCTGCA AGTCCCTGCA CTGTGCCCGC CCGGAATTC CCCATTTCGC CCCGGAATTC CTGCAGCCCG GGGGATCCAC
     TCCTCCTCTG TTCCGTCTTC CGTCGGACGT TCAGGGACGT GACACGGGCG GGCCCTTAAG GGGTAAAGCG GGCCTTAAG GACGTCGGGC CCCCTAGGTG

2001 TAGTTCTAGA GCGGCCGCCA CCGCGGTGGA GCTCCAGCTT TTGTTCCCTT TAGTGAGGGT TAATTGCGCG CTTGGGTATC TT
     ATCAAGATCT CGCCGGCGGT GGCGCCACCT CGAGGTCGAA AACAAGGGAA ATCACTCCCA ATTAACGCGC GAACCCATAG AA

FIG. 11B